

-77-

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT(S): HOGREFE, Holly
HANSEN, Connie J
- (ii) TITLE OF INVENTION: Polymerase Enhancing Factor (PEF)
Extracts, PEF Protein Complexes,
Isolated PEF Proteins, and Methods for
Purifying and Identifying Them
- (iii) NUMBER OF SEQUENCES: 89
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: M. Paul Barker, Esq., Finnegan,
Henderson, Farabow, Garrett & Dunner, LLP
- (B) STREET: 1300 I. Street, N.W.
- (C) CITY: Washington
- (D) STATE: DC
- (F) ZIP: 20005
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: NOT YET KNOWN
- (B) FILING DATE: 20-MARCH-1998
- (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: BARKER, M. PAUL
- (B) REGISTRATION NUMBER: 32,013
- (C) REFERENCE/DOCKET NUMBER: 4121.0116.02304
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 202 408-4000
- (B) TELEFAX: 202 408-4400

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Xaa Xaa Leu His His Val Lys Leu Ile Tyr Ala Thr Xaa Xaa Xaa
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

-78-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Xaa Xaa Xaa Pro Asp Trp Xaa Xaa Arg Xaa Glu Xaa Leu Xaa Xaa
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Xaa Leu Leu His His Val Lys Leu Ile Tyr Ala Thr Lys Xaa Arg Xaa
 1 5 10 15
 Leu Val Gly Lys Xaa Ile Val Leu Ala Ile Pro Gly Xaa Xaa Ala Xaa
 20 25 30
 Xaa Xaa Xaa
 35

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Xaa Xaa Xaa Pro Asp Trp Xaa Xaa Arg Xaa Glu Xaa Leu Xaa Glu Xaa
 1 5 10 15
 Xaa Xaa

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Xaa Tyr Asp Ala Val Ile Met Ala Ala Val Val Asp Phe Arg Pro
 1 5 10 15
 Lys

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

-79-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Asp Leu Val Val Gly Asn Thr Leu Glu Ala Phe Gly Ser Glu Glu

1 5 10 15

Asn Gln Val Val Leu Ile Gly Arg

20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Ala Met Leu His His Val Lys Leu Ile Tyr Ala Xaa Lys Leu Arg

1 5 10 15

Lys

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gly Ala Met Leu His His Val Lys Leu Ile Tyr Ala Thr Lys Xaa Xaa

1 5 10 15

Arg Lys

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Leu His His Val Lys Leu Ile Tyr Ala Thr Lys Leu

1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly Xaa Xaa Xaa Pro Asp Trp Xaa Xaa Lys Phe Arg Lys Glu Glu Ser

-80-

- 1 5 10 15
- (2) INFORMATION FOR SEQ ID NO:11:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
- Gly Ala Ile Leu Leu Pro Asp Trp Lys Ile Arg Lys Glu Ile Leu Ile
- 1 5 10 15
- Glu
- 15
- (2) INFORMATION FOR SEQ ID NO:12:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
- Xaa Met His His Val Ile Lys Leu Xaa Tyr Ala Thr Xaa Ser Arg Lys
- 1 5 10 15
- (2) INFORMATION FOR SEQ ID NO:13:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
- Met Leu Tyr Leu Val Arg Pro Asp Trp Lys Arg Arg Lys Glu Ile Leu
- 1 5 10 15
- Ile Glu
- 40
- (2) INFORMATION FOR SEQ ID NO:14:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
- CAYCAYGAHA ARYTHATTTA CGC
- 50
- (2) INFORMATION FOR SEQ ID NO:15:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid

23

-81-

(C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: YES
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
 GCCATDATNA CDGCRTCGTA TTT 23

(2) INFORMATION FOR SEQ ID NO:16:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
 CAYCAYGAHA ARYTHATATA CGC 23

(2) INFORMATION FOR SEQ ID NO:17:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: YES
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
 ARDACDACYT GRTTTTCTTC 20

(2) INFORMATION FOR SEQ ID NO:18:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATGCTTCACC	ACGTCAAGCT	AATCTACGCC	ACAAAAAGTC	GAAAGCTAGT	TGGAAAAAAG	60
ATAGTCNNNN	NNNNNCCAGG	GAGTATTGCG	GCTTTGGATG	TGAAAGCTTG	TGAGGGACTA	120
ATTAGGCATG	GGGCCGAAGT	TCATGCAGTG	ATGAGTGAGG	CAGCCACCAA	GATAATTCAT	180
CCTTATGCAT	GGAATTTGCC	CACGGGAAAT	CCAGTCATAA	CTGAGATCAC	TGGATTTATC	240
GAGCATGTTG	AGTTAGCAGG	GGAACATGAG	AATAAAGCAG	ATTTAATTTT	GGTTTGTCTT	300
GCCACTGCCA	ACACAATTAG	TAAGATTGCA	TGTGGAATAG	ATGATACTCC	AGTAACTACA	360
GTCGTGACCA	CAGCATTTC	CCACATTCCA	ATTATGATAG	CCCCAGCAAT	GCATGAGACA	420
ATGTACAGGC	ATCCCATAGT	AAGGGAGAAC	ATTGAAAGGT	TAAAGAAGCT	TGGCGTTGAG	480
TTTATAGGAC	CAAGAATTGA	GGAGGGAAAG	GCAAAAGTTG	CAAGCATTGA	TGAAATAGTT	540
TACAGAGTTA	TTAAAAAGCT	CCACAAAAAA	ACATTGGAAG	GGAAGAGAGT	CCTAGTAACG	600
GCGGGAGCAA	CAAGAGAGTA	CATAGATCCA	ATAAGATTCA	TAACAAATGC	CAGCAGTGGA	660
AAAATGGGAG	TAGCGTTGGC	TGAAGAAGCA	GATTTTAGAG	GAGCTGTTAC	CCTCATAAGA	720
ACAAAGGGAA	GTGTAAAGGC	TTTTAGAATC	AGAAAAATCA	AATTGAAGGT	TGAGACAGTG	780
GAAGAAATGC	TTTCAGCGAT	TGAAAATGAG	TTGAGGAGTA	AAAAGTATGA	CGTAGTTATT	840
ATGGCAGCTG	CTGTAAGCGA	TTTTAGGCCA	AAAATTAAAG	CAGAGGGAAA	AATTAAAAGC	900

-82-

GGAAGATCAA TAACGATAGA GCTCGTTCCN NNNAAATCCCA AAATCATTGA TAGAATAAAG 960
 GAAATTCAAC CAAATGTCTT TCTTGTTGGA TTTAAAGCAG AAACCTTCAA AGAAAAGCTT 1020
 ATAGAAGAAG GTAAAAGGCA GATTGAGAGG GCCAAGGCTG ACTTAGTCGT TGGTAACACA 1080
 TTGGAAGCCT TTGGAAGCGA GGAAAACCAA GTAGTATTAA TTGGCAGAGA TTTACAAAAA 1140
 GAACTTCCAA AAATGAAAAA GAGAGAGTTA GCAGAGAGAA TTTGGGATGA GATAGAGAAA 1200
 TTNCTGTCC 1209

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 403 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met	Leu	His	His	Val	Lys	Leu	Ile	Tyr	Ala	Thr	Lys	Ser	Arg	Lys	Leu	1	5	10	15
Val	Gly	Lys	Lys	Ile	Val	Xaa	Xaa	Xaa	Pro	Gly	Ser	Ile	Ala	Ala	Leu	20	25	30	
Asp	Val	Lys	Ala	Cys	Glu	Gly	Leu	Ile	Arg	His	Gly	Ala	Glu	Val	His	35	40	45	
Ala	Val	Met	Ser	Glu	Ala	Ala	Thr	Lys	Ile	Ile	His	Pro	Tyr	Ala	Trp	50	55	60	
Asn	Leu	Pro	Thr	Gly	Asn	Pro	Val	Ile	Thr	Glu	Ile	Thr	Gly	Phe	Ile	65	70	75	80
Glu	His	Val	Glu	Leu	Ala	Gly	Glu	His	Glu	Asn	Lys	Ala	Asp	Leu	Ile	85	90	95	
Leu	Val	Cys	Pro	Ala	Thr	Ala	Asn	Thr	Ile	Ser	Lys	Ile	Ala	Cys	Gly	100	105	110	
Ile	Asp	Asp	Thr	Pro	Val	Thr	Thr	Val	Val	Thr	Thr	Ala	Phe	Pro	His	115	120	125	
Ile	Pro	Ile	Met	Ile	Ala	Pro	Ala	Met	His	Glu	Thr	Met	Tyr	Arg	His	130	135	140	
Pro	Ile	Val	Arg	Glu	Asn	Ile	Glu	Arg	Leu	Lys	Lys	Leu	Gly	Val	Glu	145	150	155	160
Phe	Ile	Gly	Pro	Arg	Ile	Glu	Glu	Gly	Arg	Ala	Lys	Val	Ala	Ser	Ile	165	170	175	
Asp	Glu	Ile	Val	Tyr	Arg	Val	Ile	Lys	Lys	Leu	His	Lys	Lys	Thr	Leu	180	185	190	
Glu	Gly	Lys	Arg	Val	Leu	Val	Thr	Ala	Gly	Ala	Thr	Arg	Glu	Tyr	Ile	195	200	205	
Asp	Pro	Ile	Arg	Phe	Ile	Thr	Asn	Ala	Ser	Ser	Gly	Lys	Met	Gly	Val	210	215	220	
Ala	Leu	Ala	Glu	Glu	Ala	Asp	Phe	Arg	Gly	Ala	Val	Thr	Leu	Ile	Arg	225	230	235	240
Thr	Lys	Gly	Ser	Val	Lys	Ala	Phe	Arg	Ile	Arg	Lys	Ile	Lys	Leu	Lys	245	250	255	
Val	Glu	Thr	Val	Glu	Glu	Met	Leu	Ser	Ala	Ile	Glu	Asn	Glu	Leu	Arg	260	265	270	
Ser	Lys	Lys	Tyr	Asp	Val	Val	Ile	Met	Ala	Ala	Ala	Val	Ser	Asp	Phe	275	280	285	
Arg	Pro	Lys	Ile	Lys	Ala	Glu	Gly	Lys	Ile	Lys	Ser	Gly	Arg	Ser	Ile	290	295	300	
Thr	Ile	Glu	Leu	Val	Pro	Xaa	Asn	Pro	Lys	Ile	Ile	Asp	Arg	Ile	Lys				

-83-

305 310 315 320
 Glu Ile Gln Pro Asn Val Phe Leu Val Gly Phe Lys Ala Glu Thr Ser
 325 330 335
 Lys Glu Lys Leu Ile Glu Glu Gly Lys Arg Gln Ile Glu Arg Ala Lys
 340 345 350
 Ala Asp Leu Val Val Gly Asn Thr Leu Glu Ala Phe Gly Ser Glu Glu
 355 360 365

 Asn Gln Val Val Leu Ile Gly Arg Asp Phe Thr Lys Glu Leu Pro Lys
 370 375 380
 Met Lys Lys Arg Glu Leu Ala Glu Arg Ile Trp Asp Glu Ile Glu Lys
 385 390 395 400
 Xaa Leu Ser

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CATAGCGAAT TCGCAAAACC TTTCGCGGTA TGG

33

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ACTACGGAAT TCCACGGAAA ATGCCGCTCA TCC

33

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGCGTTTCCG TTCTTCTTCG

20

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

-84-

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CCATCTCACG CGCCAGTTTC

20

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAGGAGAGCA GGAAAGGTGG AAC

23

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCTGGGAGAA GACTTCACTG G

21

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GAGCTTGCTC AACTTTATC

19

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GATAGAGATA GTTTCTGGAG ACG

23

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

-85-

(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: YES
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:
CGGGATATCG ACATTCTGC ACC 23

(2) INFORMATION FOR SEQ ID NO:29:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: YES
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:
GAGTTAAATG CCTACACTGT ATCT 24

(2) INFORMATION FOR SEQ ID NO:30:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:
CAGGACTCAG AAGCTGCTAT CGAA 24

(2) INFORMATION FOR SEQ ID NO:31:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:
CTGCACGTGC CCTGTAGGAT TTGT 24

(2) INFORMATION FOR SEQ ID NO:32:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
CCAGAYTGGA ARWKNAGGAA AGA 23

(2) INFORMATION FOR SEQ ID NO:33:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

-86-

(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
CCAGAYTGGA ARWKNAGAAA AGA 23
(2) INFORMATION FOR SEQ ID NO:34:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:
CCAGAYTGGA ARWKNAGGAA GGA 23
(2) INFORMATION FOR SEQ ID NO:35:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:
CCAGAYTGGA ARWKNAGAAA GGA 23
(2) INFORMATION FOR SEQ ID NO:36:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:
CAGAGTGGGC AGAGAGGCTN TTGTTAAGGG GAAATTAATC GACGTGGAAA 60
AGGAAGGAAA 84
AGTCGNTATT CCTCCAAGGG AATA 84
(2) INFORMATION FOR SEQ ID NO:37:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL: YES
(iv) ANTI-SENSE: NO
(v) FRAGMENT TYPE: internal
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:
Glu Trp Ala Glu Arg Leu Leu Leu Arg Gly Asn Xaa Ser Lys Trp Lys
1 5 10 15

-87-

Arg Lys Glu Lys Ser Xaa Phe Leu Gln Gly Asn
20 25

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Arg Val Gly Arg Glu Ala Xaa Val Lys Gly Lys Leu Ile Glu Val Glu
1 5 10 15
Lys Glu Gly Lys Val Xaa Ile Pro Pro Arg Glu
20 25

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Gln Ser Gly Gln Arg Gly Xaa Cys Xaa Gly Glu Ile Asn Arg Ser Gly
1 5 10 15
Lys Gly Arg Lys Ser Arg Tyr Ser Ser Lys Gly Leu
20 25

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CTGCCCCACTC TGAGGTCATA ACCTGCTGGT TGGAGCCATT CTTGAGAAAA TGGCTCTATA 60
AGTATTTCTT TTCTGATTTT CCAGTCTGGA AGTAGCATT TACCACCGAA ACCTTTATTT 120
TTAATTAA 129

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Xaa Ile Lys Asn Lys Gly Phe Gly Gly Lys Met Leu Leu Pro Asp Trp

-88-

1 5 10 15
 Lys Ile Arg Lys Glu Ile Leu Ile Glu Pro Phe Ser Glu Glu Trp Leu
 20 25 30
 Gln Pro Ala Gly Tyr Asp Leu Arg Val Gly
 35 40

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TCCTCCAAGG GAATACGCCT TAATCCTAAC CCTCGAGAGG ATAAAGTTGC CCGACGATGT 60
 TATGGGGGAT ATGAAGATAA GGAGCAGTTT AGCAAGAGAA GGGGTTATTG GTTCTTTTGC 120
 TTGGGTTGAC CCAGGATGGG ATGGAACTT AACACTAATG CTCTACAATG CCTCAAATGA 180
 ACCTGTGCGAA TTAAGATATG GAGAGAGATT TGTGCAGATC GCATTTATAA GGCTAGAGGG 240
 TCCGGCAAGA AACCCTTACA GAGGAACTA TCAGGGGAGC ACAAGGTTAG CGTTTTCAAA 300
 GAGAAAGAAA CTCTAGCGTC TTTTCAATAG CATCCTCAAT ATCTCGTGTG AAGTAATCAA 360
 TGTAATAACT TGCTGGGTGG GTTTTTAGGG ATTCAACTC GTAAGATGGG CCTGTATAGC 420
 AGAAAACCTAT TTTTGCCTCT TCTTCATTTA TCTTCTGTG AATAAAAAAT CCAACATCCA 480
 CACTAGTTCC AAAAGATATT GTTTGCGTGA TTACCAACAA GATCTTGGCA TTATTTTGA 540
 TCTTATACTC TATTCTCCTT TCTCCCTCCA ATTTGCCCAA AATAAACCTG GG TAGTATAC 600
 ATTCACTCCT CTCTTTTAAA TTCCTATAAA TTCGTACATA GTTTAGAAAA ATGTCAAATT 660
 CTTTNTTCCC TGTTAAATTA ACCNCNAAAT CTTTATNANN AANCTTTTTA TAATCCCAA 720
 AACCCTAAT TTTCCCCTTN 740

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Leu Gln Gly Asn Thr Pro Xaa Ser Xaa Pro Ser Arg Gly Xaa Ser Cys
 1 5 10 15
 Pro Thr Met Leu Trp Gly Ile Xaa Arg Xaa Gly Ala Val Xaa Gln Glu
 20 25 30
 Lys Gly Leu Val Leu Leu Leu Gly Leu Thr Gln Asp Gly Met Glu
 35 40 45
 Thr Xaa His Xaa Cys Ser Thr Met Pro Gln Met Asn Leu Ser Asn Xaa
 50 55 60
 Asp Met Glu Arg Asp Leu Cys Arg Ser His Leu Xaa Gly Xaa Arg Val
 65 70 75 80
 Arg Gln Glu Thr Leu Thr Glu Glu Thr Ile Arg Gly Ala Gln Gly Xaa
 85 90 95
 Arg Phe Gln Arg Glu Arg Asn Ser Ser Val Phe Ser Ile Ala Ser Ser
 100 105 110
 Ile Ser Arg Val Lys Xaa Ser Met Xaa Ile Leu Ala Gly Trp Val Phe

-89-

	115		120		125
Arg	Asp	Ser	Asn	Ser	Xaa
130			135		140
Ala	Ser	Ser	Ser	Phe	Ile
145			150		155
Leu	Val	Pro	Lys	Asp	Ile
			165		170
Leu	Phe	Leu	Ile	Leu	Tyr
			180		185
Lys	Ile	Asn	Leu	Gly	Ser
			195		200
Xaa	Ile	Arg	Thr	Xaa	Phe
			210		215
Lys	Leu	Thr	Xaa	Lys	Ser
225			230		235
Pro	Leu	Ile	Phe	Pro	Xaa
			245		

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Pro	Pro	Arg	Glu	Tyr	Ala	Leu	Ile	Leu	Thr	Leu	Glu	Arg	Ile	Lys	Leu
1			5					10						15	
Pro	Asn	Asn	Val	Met	Gly	Asp	Met	Lys	Ile	Arg	Ser	Ser	Leu	Ala	Arg
			20					25						30	
Glu	Gly	Val	Ile	Gly	Ser	Phe	Ala	Trp	Val	Asp	Pro	Gly	Trp	Asp	Gly
			35					40						45	
Asn	Leu	Thr	Leu	Met	Leu	Tyr	Asn	Ala	Ser	Asn	Glu	Pro	Val	Glu	Leu
			50					55						60	
Arg	Tyr	Gly	Glu	Arg	Phe	Val	Gln	Ile	Ala	Phe	Ile	Arg	Leu	Glu	Gly
65								70						75	
Pro	Ala	Arg	Asn	Pro	Tyr	Arg	Gly	Asn	Tyr	Gln	Gly	Ser	Thr	Arg	Leu
								85						90	
Ala	Phe	Ser	Lys	Arg	Lys	Lys	Leu	Xaa	Arg	Leu	Phe	Asn	Ser	Ile	Leu
			100					105						110	
Asn	Ile	Ser	Cys	Glu	Val	Ile	Asn	Val	Asn	Thr	Cys	Trp	Val	Gly	Phe
			115					120						125	
Xaa	Gly	Phe	Lys	Leu	Val	Arg	Trp	Ala	Cys	Ile	Ala	Glu	Asn	Tyr	Phe
			130					135						140	
Cys	Leu	Phe	Phe	Ile	Tyr	Leu	Ser	Val	Asn	Lys	Lys	Ser	Asn	Ile	His
145								150						155	
Thr	Ser	Ser	Lys	Arg	Tyr	Cys	Leu	Arg	Asp	Tyr	Gln	Gln	Asp	Leu	Gly
								165						170	
Ile	Ile	Phe	Asp	Leu	Ile	Leu	Tyr	Ser	Pro	Phe	Ser	Leu	Gln	Phe	Ala
								180						185	
Gln	Asn	Lys	Pro	Gly	Xaa	Tyr	Thr	Phe	Thr	Pro	Leu	Phe	Xaa	Ile	Pro
								195						200	
Ile	Asn	Ser	Tyr	Ile	Val	Xaa	Lys	Asn	Val	Lys	Phe	Phe	Xaa	Pro	Cys
								210						215	
														220	

-90-

Xaa Ile Asn Xaa Xaa Ile Phe Xaa Xaa Xaa Leu Phe Ile Ile Pro Lys
 225 230 235 240
 Thr Pro Asn Phe Pro Leu
 245

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Ser Ser Lys Gly Ile Arg Leu Asn Pro Asn Pro Arg Glu Asp Lys Val
 1 5 10 15
 Ala Arg Arg Cys Tyr Gly Gly Tyr Glu Asp Lys Glu Gln Phe Ser Lys
 20 25 30
 Arg Arg Gly Tyr Trp Phe Phe Cys Leu Gly Xaa Pro Arg Met Gly Trp
 35 40 45
 Lys Leu Asn Thr Asn Ala Leu Gln Cys Leu Lys Xaa Thr Cys Arg Ile
 50 55 60
 Lys Ile Trp Arg Glu Ile Cys Ala Asp Arg Ile Tyr Lys Ala Arg Gly
 65 70 75 80
 Ser Gly Lys Lys Pro Leu Gln Arg Lys Leu Ser Gly Glu His Lys Val
 85 90 95
 Ser Val Phe Lys Glu Lys Glu Thr Leu Ala Ser Phe Gln Xaa His Pro
 100 105 110
 Gln Tyr Leu Val Xaa Ser Asn Gln Cys Lys Tyr Leu Leu Gly Gly Phe
 115 120 125
 Leu Gly Ile Gln Thr Arg Lys Met Gly Leu Tyr Ser Arg Lys Leu Phe
 130 135 140
 Leu Pro Leu Leu His Leu Ser Phe Cys Glu Xaa Lys Ile Gln His Pro
 145 150 155 160
 His Xaa Phe Gln Lys Ile Leu Phe Ala Xaa Leu Pro Thr Arg Ser Trp
 165 170 175
 His Tyr Phe Xaa Ser Tyr Thr Leu Phe Ser Phe Leu Pro Pro Ile Cys
 180 185 190
 Pro Lys Xaa Thr Trp Val Val Tyr Ile His Ser Ser Leu Leu Asn Ser
 195 200 205
 Tyr Lys Phe Val His Ser Leu Glu Lys Cys Gln Ile Leu Xaa Ser Leu
 210 215 220
 Leu Asn Xaa Pro Xaa Asn Leu Tyr Xaa Xaa Xaa Phe Tyr Asn Ser Gln
 225 230 235 240
 Asn Pro Xaa Phe Ser Pro
 245

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

-91-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Leu His His Val Lys Leu Ile Tyr Ala Thr Lys Ser Arg Lys Leu
 1 5 10 15
 Val Gly Lys Lys Ile Val Xaa Xaa Xaa Pro Gly Ser Ile Ala Ala
 20 25 30

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Lys Tyr Asp Val Val Ile Met Ala Ala Ala Val Ser Asp Phe Arg Phe
 1 5 10 15
 Lys

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Ala Asp Leu Val Val Gly Asn Thr Leu Glu Ala Phe Gly Ser Glu Glu
 1 5 10 15
 Asn Gln Val Val Leu Ile Gly Arg
 20

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTATTGAGTA CGAACGCCAT C

21

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

-92-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:
GTCACGCTTG CTCCACTCCG

20

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 437 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Methanococcus Jannaschii

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met	Ile	Ser	Glu	Ile	Met	His	Pro	Thr	Lys	Leu	Leu	Lys	Gly	Thr	Lys
1				5					10					15	
Ser	Lys	Leu	Leu	Glu	Asn	Lys	Lys	Ile	Leu	Val	Ala	Val	Thr	Ser	Ser
			20					25					30		
Ile	Ala	Ala	Ile	Glu	Thr	Pro	Lys	Leu	Met	Arg	Glu	Leu	Ile	Arg	His
		35					40					45			
Gly	Ala	Glu	Val	Tyr	Cys	Ile	Ile	Thr	Glu	Glu	Thr	Lys	Lys	Ile	Ile
	50					55					60				
Gly	Lys	Glu	Ala	Leu	Lys	Phe	Gly	Cys	Gly	Asn	Glu	Val	Tyr	Glu	Glu
65					70					75					80
Ile	Thr	Gly	Xaa	Xaa	Xaa	Xaa	Xaa	Asp	Ile	Glu	His	Ile	Leu	Leu	Tyr
			85					90					95		
Xaa	Xaa	Xaa	Xaa	Asn	Glu	Cys	Asp	Cys	Leu	Leu	Ile	Tyr	Pro	Ala	Thr
			100					105					110		
Ala	Asn	Ile	Ile	Ser	Lys	Ile	Asn	Leu	Gly	Ile	Ala	Asp	Asn	Ile	Val
		115					120					125			
Asn	Thr	Thr	Ala	Leu	Met	Phe	Phe	Gly	Asn	Lys	Pro	Ile	Phe	Ile	Val
	130					135					140				
Pro	Ala	Met	His	Glu	Asn	Met	Phe	Asn	Xaa	Xaa	Ala	Ile	Lys	Arg	His
145					150					155				160	
Ile	Asp	Lys	Leu	Lys	Glu	Lys	Asp	Lys	Ile	Tyr	Ile	Ile	Ser	Pro	Lys
			165					170					175		
Phe	Glu	Glu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Lys	Ala	Lys	Val	Ala	Asn
			180				185						190		
Ile	Glu	Asp	Val	Val	Lys	Ala	Val	Ile	Glu	Lys	Ile	Gly	Asn	Asn	Leu
	195						200					205			
Lys	Lys	Glu	Gly	Asn	Arg	Val	Leu	Ile	Leu	Asn	Gly	Gly	Thr	Val	Glu
	210					215					220				
Phe	Ile	Asp	Lys	Val	Arg	Val	Ile	Ser	Asn	Leu	Ser	Ser	Gly	Lys	Met
225					230					235				240	
Gly	Val	Ala	Leu	Ala	Glu	Ala	Phe	Cys	Lys	Glu	Gly	Phe	Tyr	Val	Glu
			245						250					255	
Val	Ile	Thr	Ala	Met	Gly	Leu	Glu	Pro	Pro	Tyr	Tyr	Ile	Lys	Asn	His
			260				265						270		
Lys	Val	Leu	Thr	Ala	Lys	Glu	Met	Leu	Asn	Lys	Ala	Ile	Glu	Xaa	Xaa
		275					280					285			
Leu	Xaa	Ala	Lys	Asp	Phe	Asp	Ile	Ile	Ile	Ser	Ser	Ala	Ala	Ile	Ser
	290					295					300				
Asp	Phe	Thr	Val	Glu	Ser	Xaa	Phe	Glu	Gly	Lys	Leu	Ser	Ser	Glu	Glu
305					310					315				320	
Glu	Xaa	Xaa	Xaa	Xaa	Leu	Ile	Leu	Lys	Leu	Lys	Arg	Xaa	Asn	Pro	Lys

-93-

325 330 335
 Val Leu Glu Glu Leu Arg Arg Ile Tyr Lys Asp Xaa Lys Val Ile Ile
 340 345 350
 Gly Phe Lys Ala Glu Tyr Asn Leu Asp Glu Lys Glu Leu Ile Asn Arg
 355 360 365
 Ala Lys Glu Arg Leu Asn Lys Tyr Asn Leu Asn Met Ile Ile Ala Asn
 370 375 380
 Asp Leu Ser Lys Xaa Xaa His Tyr Phe Gly Asp Asp Tyr Ile Glu Val
 385 390 395 400
 Tyr Ile Ile Thr Lys Tyr Glu Val Glu Lys Ile Ser Gly Ser Lys Lys
 405 410 415
 Xaa Glu Ile Ser Glu Arg Ile Val Glu Lys Val Lys Lys Leu Val Lys
 420 425 430
 Ser Xaa Xaa Xaa Xaa
 435

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Escherichia coli

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Lys Ala Arg Gln Gln Lys Tyr Cys Asp Lys Ile Ala Asn Phe Trp
 1 5 10 15
 Cys His Pro Thr Gly Lys Ile Ile Met Ser Leu Ala Gly Lys Lys Ile
 20 25 30
 Val Leu Gly Val Ser Gly Gly Ile Ala Ala Tyr Lys Thr Pro Glu Leu
 35 40 45
 Val Arg Arg Leu Arg Asp Arg Gly Ala Asp Val Arg Val Ala Met Thr
 50 55 60
 Glu Ala Ala Lys Ala Phe Ile Thr Pro Leu Ser Leu Gln Ala Val Ser
 65 70 75 80
 Gly Tyr Pro Val Ser Asp Ser Leu Leu Asp Pro Ala Ala Glu Ala Ala
 85 90 95
 Met Gly His Ile Glu Leu Gly Xaa Xaa Xaa Lys Trp Ala Asp Leu
 100 105 110
 Val Ile Leu Ala Pro Ala Thr Ala Asp Leu Ile Ala Arg Val Ala Ala
 115 120 125
 Gly Met Ala Asn Asp Leu Val Ser Thr Ile Cys Leu Ala Thr Pro Xaa
 130 135 140
 Xaa Ala Pro Val Ala Val Leu Pro Ala Met Asn Gln Gln Met Tyr Arg
 145 150 155 160
 Ala Ala Ala Thr Gln His Asn Leu Glu Val Leu Ala Xaa Ser Arg Gly
 165 170 175
 Leu Leu Ile Trp Gly Pro Asp Ser Gly Ser Gln Ala Cys Gly Asp Ile
 180 185 190
 Gly Pro Gly Arg Xaa Xaa Asp Pro Leu Thr Ile Val Asp Met Ala Val
 195 200 205
 Ala His Phe Ser Pro Val Asn Asp Leu Lys His Leu Asn Ile Met Ile
 210 215 220

-94-

Thr Ala Gly Pro Thr Arg Glu Pro Leu Asp Pro Val Arg Tyr Ile Ser
 225 230 235 240
 Asn His Ser Ser Gly Lys Met Gly Phe Ala Ile Ala Ala Ala Ala
 245 250 255
 Arg Arg Gly Ala Asn Val Thr Leu Val Ser Gly Pro Val Ser Leu Pro
 260 265 270
 Thr Pro Pro Phe Val Lys Arg Val Asp Val Met Thr Ala Leu Glu Met
 275 280 285
 Glu Ala Ala Val Asn Xaa Xaa Ala Ser Val Gln Gln Asn Ile Phe
 290 295 300
 Ile Gly Cys Ala Ala Val Ala Asp Tyr Arg Ala Ala Thr Val Ala Pro
 305 310 315 320
 Glu Lys Ile Lys Lys Gln Ala Thr Gln Gly Asp Glu Leu Thr Ile Lys
 325 330 335
 Met Val Lys Xaa Asn Pro Asp Ile Val Ala Gly Val Ala Ala Leu Lys
 340 345 350
 Asp His Arg Pro Tyr Val Val Gly Phe Ala Ala Glu Thr Asn Asn Xaa
 355 360 365
 Xaa Xaa Xaa Val Glu Glu Tyr Ala Arg Gln Lys Arg Ile Arg Lys Asn
 370 375 380
 Leu Asp Leu Ile Cys Ala Asn Asp Val Ser Gln Pro Thr Gln Gly Phe
 385 390 395 400
 Asn Ser Asp Asn Asn Ala Leu His Leu Phe Trp Gln Asp Gly Asp Lys
 405 410 415
 Val Leu Pro Leu Glu Arg Lys Glu Leu Gly Gln Leu Leu Leu Asp
 420 425 430
 Glu Ile Val Thr Arg Tyr Asp Glu Lys Asn Arg Arg
 435 440

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Xaa Gly Xaa Xaa Asp Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa
 1 5 10

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Phe Ala Trp Val Asp Pro Gly Trp Asp Gly Asn Thr Leu Met
 1 5 10

-95-

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala Gly Trp Ile Asp Ala Gly Phe Lys Gly Lys Ile Thr Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ser Ala Val His Asp Pro Gly Tyr Glu Gly Arg Pro Glu Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Pro Thr Ile Val Asp Ala Gly Phe Glu Gly Gln Leu Thr Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Ala His Arg Ile Asp Pro Gly Trp Ser Gly Cys Ile Val Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

-96-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:
GAGTTAAATG CCTACACTGT ATCT 24

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:
CAGGACTCAG AAGCTGCTAT CGAA 24

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:
CTGCACGTGC CCTGTAGGAT TTGT 24

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:
CTATTGAGTA CGAACGCCAT C 21

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:
GTCACGCTTG CTCCACTCCG 20

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

-97-

(iv) ANTI-SENSE: NO
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:
GAGGAGAGCA GGAAAGGTGG AAC

23

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GCTGGGAGAA GACTTCACTG G

21

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

His His Val Lys Leu Ile Tyr Ala

1

5

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Lys Tyr Asp Ala Val Ile Met Ala

1

5

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Glu Glu Asn Gln Val Val Leu

1

5

(2) INFORMATION FOR SEQ ID NO:69:

-98-

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Pro Asp Trp Lys Ile Arg Lys Glu

1

5

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ATGCTACTTC CAGACTGGAA AATCAGAAAA GAAATACTTA TAGAGCCATT TTCTGAAGAA 60
 TCGCTCCAAC CAGCAGGTTA TGACCTCAGA GTGGGCAGAG AGGCTTTTGT TAAGGGGAAA 120
 TTAATCGACG TGGAAAAGGA AGGAAAAGTC GTTATTCCTC CAAGGGAATA CGCCTTAATC 180
 CTAACCCTCG AGAGGATAAA GTTGCCCGAC GATGTTATGG GGGATATGAA GATAAGGAGC 240
 AGTTTAGCAA GAGAAGGGGT TATTGGTTCT TTTGCTTGGG TTGACCCAGG ATGGGATGGA 300
 AACTTAACAC TAATGCTCTA CAATGCCTCA AATGAACCTG TCGAATTAAG ATATGGAGAG 360
 AGATTTGTGC AGATCGCATT TATAAGGCTA GAGGGTCCGG CAAGAAACCC TTACAGAGGA 420
 AACTATCAGG GGAGCACAAG GTTAGCGTTT TCAAAGAGAA AGAAACTCTA G 471

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Met Leu Leu Pro Asp Trp Lys Ile Arg Lys Glu Ile Leu Ile Glu Pro
 1 5 10 15
 Phe Ser Glu Glu Ser Leu Gln Pro Ala Gly Tyr Asp Leu Arg Val Gly
 20 25 30
 Arg Glu Ala Phe Val Lys Gly Lys Leu Ile Asp Val Glu Lys Glu Gly
 35 40 45
 Lys Val Val Ile Pro Pro Arg Glu Tyr Ala Leu Ile Leu Thr Leu Glu
 50 55 60
 Arg Ile Lys Leu Pro Asp Asp Val Met Gly Asp Met Lys Ile Arg Ser
 65 70 75 80
 Ser Leu Ala Arg Glu Gly Val Ile Gly Ser Phe Ala Trp Val Asp Pro
 85 90 95
 Gly Trp Asp Gly Asn Leu Thr Leu Met Leu Tyr Asn Ala Ser Asn Glu
 100 105 110

-99-

Pro Val Glu Leu Arg Tyr Gly Glu Arg Phe Val Gln Ile Ala Phe Ile
115 120 125
Arg Leu Glu Gly Pro Ala Arg Asn Pro Tyr Arg Gly Asn Tyr Gln Gly
130 135 140
Ser Thr Arg Leu Ala Phe Ser Lys Arg Lys Lys Leu
145 150 155

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Xaa Gly Xaa Xaa Asp Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Phe Ala Trp Val Asp Pro Gly Trp Asp Gly Asn Thr Leu Met
1 5 10

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Ala Gly Trp Ile Asp Ala Gly Phe Lys Gly Lys Ile Thr Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

-100-

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Ser Ala Val His Asp Pro Gly Tyr Glu Gly Arg Pro Glu Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Pro Thr Ile Val Asp Ala Gly Phe Glu Gly Gln Leu Thr Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Ala His Arg Ile Asp Pro Gly Trp Ser Gly Cys Ile Val Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Val Gly Leu Ile Asp Ser Asp Tyr Gln Gly Gln Leu Met Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

-101-

- (v) FRAGMENT TYPE: internal
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:
Ala Gly Val Val Asp Arg Asp Tyr Thr Gly Glu Val Lys Val
1 5 10
- 5 (2) INFORMATION FOR SEQ ID NO:80:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
10 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(v) FRAGMENT TYPE: internal
15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:
Ala Gly Val Ile Asp Glu Asp Tyr Arg Gly Asn Val Gly Val
1 5 10
- 20 (2) INFORMATION FOR SEQ ID NO:81:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
25 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(v) FRAGMENT TYPE: internal
30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:
Thr Gly Leu Ile Asp Pro Gly Phe Gln Gly Glu Leu Lys Leu
1 5 10
- 35 (2) INFORMATION FOR SEQ ID NO:82:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
40 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:
GACGACGACA AGATGCTACT TCCAGACTGG AAA 33
- 45 (2) INFORMATION FOR SEQ ID NO:83:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
50 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:
GGAACAAGAC CCGTCCCACT TTCACAGATG AAGAG 35
- (2) INFORMATION FOR SEQ ID NO:84:
(i) SEQUENCE CHARACTERISTICS:

-102-

(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:
GAGGAGAGCA GGAAAGGTGG AAC 23
(2) INFORMATION FOR SEQ ID NO:85:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: YES
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:
CTCCATGTCC CAACTCCGAT CAC 23
(2) INFORMATION FOR SEQ ID NO:86:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:
GGTTTTCCCA GTCACGACGT TGTAACACGA CGGCCAGT 38
(2) INFORMATION FOR SEQ ID NO:87:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:
GGUUUCCCA GUCACGACGU UGUAAAACGA CGGCCAGU 38
(2) INFORMATION FOR SEQ ID NO:88:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:
GACGACGACA AGATGCCCTG CTCTGAAGAG ACACC 35
(2) INFORMATION FOR SEQ ID NO:89:

-103-

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: YES
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:
GGAACAAGAC CCGTTTAATT CTTCCAGTG GAACC

35